PATENT APPLICATION

TITLE :

Methods for diagnosing in vitro pathologies associated with gene rearrangement and diagnosis kits.

The invention relates to the detection of gene rearrangements with exchanges of genetic material. Said rearrangements correspond to the formation of fusion genes through coupling of the translocated part with a genome portion located on the chromosomal partner, or through modification of regulation in a gene expression. As used herein, the word "gene" will mean the gene involved in various rearrangements, while the expression "fusion partners" will make reference to the genome portions coupled with the said gene

The invention is more specifically aimed at defining a method and kits for in vitro diagnostic of pathologies associated with such rearrangements.

As regards for example leukemias, they are known to be associated with rearrangements of numerous genes, some of which recurrent like the MLL gene.

The MLL gene belongs to the 11q23 chromosomal band of human genome, frequently involved in molecular rearrangements, particularly in acute lymphoblastic leukemia (LAL) and acute myeloid leukemia (LAM) as well.

So far, by cytogenetic assessments it was possible to count about thirty different chromosomal partner bands. Thirteen MLL fusion partners have now been cloned and sequenced, which accounts for 95 % approximately of known rearrangements

In most cases, such rearrangements are associated with grim clinical prognosis , whence the emphasis placed on their evaluation in recent years.

With the development of karyotypes, cytogenetics is one of the methods used conventionally. By this technique it was possible to disclose a large number of rearrangements with a large number of partners in the 11q23 chromosomal band and to assess the prognosis significance of the anomaly. But it comprises numerous false negatives and its success rate does not exceed 50 to 70 % range

The "Southern blot" and *in situ* hybridization are amongst the other known techniques.

The Southern blot technique offers the advantage of highlighting all rearrangements but is hardly usable by clinical laboratories due to its time-consuming, heavy process and because of radioactivity constraints. In fact, therapy decisions demand results within weeks on a case by case basis.

In situ (FISH) hybridization may *a priori* highlight genetic anomalies, however its sensitivity is not always adequate due to the frequent deletions which are often found with translocations, the use of this technique may also yield false negative results.

In WO 96/13514, the characterisation and isolation of the TCL-1 gene associated with anomalies is disclosed.

This document aims to characterise all genes of the TCL-1 family and for this, uses a PCR technique that employs degenerated primers.

In the J.Clin, Pathol, 1993, 100, p 527-533, Ratech et al report the interest of anchored PCR to detect a wide spectrum of mature B Cell neoplasma. The described primers are specific to IgH and are not therefore entirely random. In addition, the PCR products obtained are cloned and sequenced, which are very labor intensive characterization techniques.

In Human genetics, 1997, 99, p 237-247, Kehrer - Sawatzki et al analyse the breakpoint regions in the NF1 gene implicated in the type 1 neurofibromatose.

The so-called semi-specific PCR technique employed is performed in such a way as to identify the jonction fragment in the breakpoint region, and the sequence being then analysed. This article does not then teach asymetric amplification to amplify the whole fusion genes and to reveal only genes implicated in the rearrangement.

In PNAS, 1993, 90, p 8538-8542, Corral et al study breaks in the MLL of different translocations and 11q deletions with cloning of certain MLL gene partners for identification, this represents a technique that can be used in research but is not adapted for routine use.

The invention further aims at providing diagnostic kits to implement this method.

The in vitro diagnostic method according to the invention, is characterized in that a patient's DNA is subjected to at least one step of anchored PCR by completing at least one step of asymmetrical amplification, by means of a single pair of primers formed by a specific DNA primer of the gene liable to be involved in a fusion gene, and a complementary random primer, and in that such a gene is only detected in so far as it is involved in the said fusion.

It will be observed that the foregoing arrangements allow one to conveniently amplify any sequence involving the relevant gene, whatever the fusion partner, and even though the length of the sequence associated with the gene be significant. On the contrary, the detection step is specific and does not allow one to detect the gene unless rearranged with a given partner

The primers used in the amplification step are conveniently selected to meet the length, Tm and end-stability criteria, particularly in the case of long fragments' amplification.

Thus, the length of the primers must ensure a stability consistent with elongation. Convenient primers include 25 to 40 nucleotides, and specifically 30 to 35 nucleotides.

The Tm temperature at which half the DNA is in denatured form is advantageously of about 80 to 86°C,

specifically close to 80°C. The sequence base composition is to be selected in such a way as will meet this requirement.

Similarly, one should take into account the stability at the 3' and 5' ends, since the primer end subjected to elongation should be less stable than the opposite end, to avoid the initiation and elongation of non specific PCR products. It is also critical to obviate the formation of duplex and loops on the 3' end which would interfere with the proper primers matching with the DNA or cDNA sequence.

The primers as described above can easily be prepared by means of software products.

The anchored PCR strategy can be conducted on the 3' end as defined hereabove, but on the 5' end as well, in which case an artificial tail is to be added to the gene's 5' end, and can be used as a primer. To that effect the deoxyribonucleotidyltransferase terminal enzyme can be conveniently used.

Rearranged genes can be detected by means of any suitable marker.

As a general rule, specific probes of nucleotide sequences of known fusion partners are put into contact with denatured PCR products, marked for detection in conditions which promote a specific probes-PCR products interaction where a complementarity of bases is present.

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PCR products carry a marker (digoxigenine, biotin or fluorophore for example) by which they will be

detected. Such marker is carried by a desoxynucleotide embodied into the PCR products during the second amplification.

The probes can be covalently secured on a support, such as 96-well plates

Such covalent bonding can be advantageously obtained through biotinylated probe /plate-streptavidine coupling.

Alternatively, this covalent bond can be achieved by means of a probe with phosphorylated end and a carbodiimide residue on the plate or a probe modified by amine residue on one end and bonded by N-oxysuccinimide esters residues.

According to a satisfactory method, the ELISA technique is used to specifically detect such nucleotide sequences that include the gene involved in a rearrangement.

PCR products in which a marker has been incorporated are allowed to react with an itself marked antibody, directed against the PCR product markers, in conditions promoting an antigen-antibody type reaction, which is detected if present by highlighting the marker of the antibody or of a reaction in which it is involved.

According to still another method, the PCR technology which enables PCR products to be detected by hybridization of internal probe and PCR product in solution.

It will be observed that multiple PCR used with different genes marked with different markers from one

another, allow a single test to detect a plurality of rearranged genes involved in a pathology.

A detection alternative, to highlight numerous genes rearrangements on a large number of genes, in a single test, is based on the DNA chips technology and comprises using oligonucleotidic or cDNA probes secured to a miniaturized support. Each probe or hybridization unit may advantageously be individually controlled by an electric field. In another alternative, the internal probes are advantageously immunobilized on strips.

The DNA subjected to amplification advantageously corresponds to the cDNA, as obtained by reverse transcription of the RNA extracted from the sample.

Alternatively, the genome DNA extracted from the sample under investigation can be used.

The internal probes are advantageously immunobilized on strips.

According to an embodiment of the invention, a reverse transcription step (RT in short) is performed before PCR amplification, to synthesize a cDNA population from the cells' RNA in the sample investigated.

A stable nucleotide sequence at 80 to 90° C Tm is conveniently used to perform this step.

Suitable sequences include a cassette with about 40 to 60 nucleotides with 10 to 20 T-patterns on one end or, alternatively, a random repeated nucleotide pattern.

According to another embodiment of the

invention, the genome DNA or RNA, extracted from the cells of the sample under investigation are subjected to the effect of a compound with the ability to inhibit or to cleave specifically the DNA of the gene under fusion investigation. These are like PNA (polypeptidic nucleic acids) or ribozymes for example. The PCR, or RT-PCR steps as the case may be, are then performed with primers which optionally include cloning sites. The products thus obtained are then set to react with two specific probes of the gene investigated, one located upstream of the break point region ("a" probe) and one downstream ("b" probe) on the one hand, and probes prepared from known partner genes ("c" probes). A positive result on «a» probe and a negative result on «b» probe, leads to conclude to the rearrangement of the gene studied, and a negative result on "c" probes detects the absence of any known fusion product. Where new fusion genes are highlighted by the test, they can be secondarily cloned and sequenced using conventional techniques.

Therefore, this technique contributes valuable information to understand molecular events underlying the cell transformation.

According to an advantageous embodiment of the invention, implemented to detect translocations involving the MLL gene, a cDNA pool is synthesized from the RNA extracted from the sample under investigation with the aid of primers including a cassette of about 30 to 35 nucleotides, complemented by a sequence of 6 or 9 random nucleotide patterns, and an anchored PCR is

performed using a primer located on the MLL' exon 5, as specific sense primer. Where a second amplification cycle is performed, an internal sens primer is used to increase the specificity. The random primer is advantageously selected as complementary to the oligonucleotides cassette used on the reverse transcription step.

The ELISA technique is used to detect fusion transcripts if any, and entails locating equally spaced probes on the fusion partners investigated, in order to encompass all break points.

In an initial step, a specific probe of known MLL' fusion partners is made to contact denatured PCR products marked by digoxygenine in the second amplification cycle, in conditions which promote hybridization where complementarity between bases exists.

In a second step, the resulting products are put into contact with anti-digoxygenine antibodies, coupled with an enzyme with the ability to release a detectable colored product if the antibodies should be secured to PCR products, by reacting with its substrate.

Hybridization between about 37 and 50 °C for 2 to 4 hours, yields satisfactory results.

The probe-PCR products interaction is achieved at a temperature in excess of 30°C, in the 35 to 65°C range, particularly at about 55°C, for 0,5 h to 5 h, and in particular, about 1 h.

Washing conditions are selected in such a way as will produce an optimum signal/noise ratio.

The enzyme substrate is prompted to react with

the probes/ PCR products reagent mixture in the same temperature and time conditions, and the product released if any can be detected, for instance by optical density measurement.

The results obtained by this method show that fusion products of the relevant translocations are easily detected through potent signals. Such results are easier to interpret than negative tests.

So, some 95 % of MLL gene rearrangements can be detected.

In order to detect new MLL-partner gene associations, total RNAs are subjected to the action of MLL gene-specific ribozymes, before the RT-PCR, after which amplification products are made to react with a probe corresponding to the MLL' Exon 5 on the primer 3' end, and then with a still MLL gene-specific second probe, located between the ribozymes' break point and action site, and finally with known partners' probes. A positive signal in the first case and a negative one with the second probe on gene MLL suggests a MLL rearrangement, while a negative signal obtained in the third step means that no known fusion product was detected. Then a new fusion gene can be highlighted.

Alternatively, partners can be sought by implementing the above described PCR steps and RT-PCR steps as the case may be, and detecting PCR products by means of DNA chips made up with oligonucleotidic or cDNA probes secured on a miniaturized surface.

The invention also provides diagnostic kits to

implement the method defined above.

Such kits are characterized in that they include the necessary reagents to perform at least one PCR and detection test and, if required, the reverse transcription and/or reaction with agents such as ribozymes or PNAs with the capability of specifically cutting or inhibiting the gene under rearrangement investigation.

Particularly, such kits include primers for the various reactions and advantageously suitable solvents or buffers, appropriate for carrying out the reactions, particularly for hybridization and washing, and a user's notice.

Preferred kits include fusion partners-specific probes secured on a support. Such probes may for instance be secured on a plate and are such as obtained by coupling a reagent on one of their ends with a plate reagent. These are for instances biotinylated probes on the 5' end secured on streptavidine coating the wells bottom of a micro-plate.

Oligonucleotidic or cDNA probes secured on a miniaturized support (DNA chips) are alternatively used.

According to still another alternative, the internal probes are fixed on strips.

The detection technique can be standardized and alleviated for the detection of fusion genes or fusion transcripts sought, thanks to the possibility of storing such support-plates which carry the probes.

Experiments on cell lines were confirmed in

patients whose gene rearrangement type was already identified, which confirms their clinical value to obtain a molecular diagnostic and to define break points.

The value of the method contemplated by the invention is underscored in those cases, particularly AML, where no chromosomal anomaly is evidenced by cytogenetic assessment whereas a molecular rearrangement is detected by molecular biology. The method contemplated by the invention allows one to screen AML patients whose karyotype is not available or was reported as normal and to ascertain whether rearrangements associated with a pathology are present or not.

The invention is therefore particularly valuable for leukemia diagnostic.

It is also especially useful in carcinology. In particular, one can mention the solid tumor diagnostic and particularly EWS genes rearrangements in Ewing. Tumors. The method contemplated by the invention allows one to detect rearrangements of EWS/FLI1 or of other members of the ETS gene family, such as ERG, ETV1 or E1AF.

As a general rule, the invention provides the necessary tools to obtain a simple, reliable and highly sensitive diagnostic over a large number of samples. The amplification of the initial sample material is also quite valuable since this material was obtained from patients, like blood or bone marrow. A large number of probes can be tested , typically up to about 500 probes on 96-well plates.

An interesting feature of the invention will be found in the arrangements whereby the tests can be automated, especially at the detection step.

Furthermore, as already emphasized, the invention provides means to detect genes which, so far, were not identified as involved in a given disorder.

Other characteristics and advantages inherent in the invention are presented in the following examples, and by referring to figure 1A to 1C which gives the general schedule of the steps used for detecing the fusion transcripts.

Example 1 : Detection protocol of a gene rearrangement with known fusion partners.

(1) The cDNAs are synthesized from the total RNAs in the sample studied, by reverse transcription (RT), then (2) the cDNA pool is amplified by PCR and (3) the transcripts are checked for specificity. Said steps are illustrated by the schedule given on the single figure.

1. RNA Preparation

The cells from the sample studied are placed in a lysate solution with addition of Trizol^{R} (Life Technologie). Then, chloroform (20% final) is added to the resulting cell lysate, and after 5 min incubation at room temperature, the mixture is centrifugalized 15 min at 4°C and 12,000 g.

Three phases are thus obtained, viz., a colorless aqueous phase containing the RNA, a whitish

intermediate phase containing the DNA, and a red, phenolic organic phase.

Isopropanol is added to the RNA, (500 µl in 1 ml Trizol^{R}), then the compound is centrifugated for 10 min at 4°C and 12,000 g, following 10 min incubation at room temperature; the resulting precipitate is then rinsed in 1 ml of 75 % ethanol (5 min at 4°C and 7,500 g).

The precipitate is dried at room temperature before mixing in 10 µl water and processed with H RNase.

The quantity of RNA extract is calculated by measuring the optical density at 260 nm : concentration (µg/µl) = measured DO x 40 (extinction coefficient) x dilution coefficient x 10^{-3}.

2. Reverse Transcription

Superscript^{R} (Life Technologie, 18064-014) or Expand Reverse Transcrip-tase^{R} (Boehringer, 1 785 834) are used as enzymatic system, under the following application protocol:

1 µg RNA is denatured (9,5 µl volume) 10 min at 70°C, then added to the reactive mixture(10,5 µl): nucleotides (1 mM) + dTT (10mM) + primer 0,5 µM) + RNases inhibitors(20 units) + enzyme (50 units of Expand Reverse Transcriptase^{R}, 200 units of Superscript)^{R}, all in a buffer suited to either enzymatic system :

Superscript^{R} : 20 mM Tris HCl, 50 mM KCl, 5 mM $MgCl_2$

Expand Reverse Transcriptase^{R} : 50 mM Tris HCl, 40

mM KCl, 5 mM $MgCl_2$.

The cDNA synthesis is performed through the following cycle : 10 min at 20°C / 45 min at 42°C / 3 min at 99°C.

The samples are then subjected to H.RNase (Boehringer, 786 357 : 2 unites) for 10 min, at 42°C.

The cDNAs are transferred into a final volume of 60 µl (dilution to 1/3) and stored at -20°C.

3 cDNA amplification by PCR

The results so obtained are reported with ELONGASE^R (BRL, 10481-018) and Expand Long template PCR System (Boehringer, 175 9060) as enzymatic systems.

Two different amplification programs are used according to the length of the fragments :

- amplification of fragments up to 1 kb:

94°C	3 min	
94°C	30 sec	|
58°C	30 sec	| x 34
72°C	30 sec	|
16°C	∞	

- amplification of fragments in excess of 1kb

95°C	30 sec	
94°C	10 sec / 68°C	8 min x 10
94°C	10 sec / 68°C	8 min + 20 sec per cycle x20
68°C	7 min	
16°C	∞	

In all cases, the reaction takes place in a 50 µl volume adhering to the following conditions: dXTP (500 µM), sens and antisens primers (1 µM), $MgCl_2$ (3 mM), enzymes (2,5 unites), all in a 50 mM Tris HCl (pH 9,2), 16 mM $(NH_4)_2SO_4$, 2% DMSO, 0,1% Tween 20 buffer solution.

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A second amplification cycle is completed to assess long fragments, using 1 µl of product obtained from the first PCR. An internal sens primer with respect to the first cycle primer is used with an identical antisens primer ; to perform the ELISA detection , the dTTP is replaced by a dTTP + DIG-dUTP^{R} mixture(Boehringer ; 1558 706) to the 1 :19 ratio.

4. <u>ELISA detection(Boehringer kit, 1636 111) of probes / PCR products hybrids.</u>

The initial step consists in putting biotinylated specific probes of known partners into contact with PCR products and the hybrids so formed are detected in the next phase.

<u>a. hybridization</u>

With the oligo 5 software, the probes are selected on the sequences of the various partners just upstream of the break points described in each translocation. Thereafter, the probes are biotinylated on the 5' end and purified with HPLC.

- extemporaneous probes fixation on ELISA plates

10 µl of PCR products are denatured in 10 µl alkaline solution, then settled in a well with streptavidine coating in the presence of the 7,5 pmol/ml biotinylated probe (220 µl end volume). The hybridization reaction takes place between 37 and 50°C, for three hours under

stirring.

The anti-DIG anti-body coupled with peroxydase (2 mU in 200 µl volume) is added after three washings, followed by 30 min incubation at 37°C and by a series of three washings.

1 mg/ml.peroxydase substrate is added (30 min et 37°C). The optical density is then read at 405 nm instead of 492 nm.

- *preliminary fixation of biotinylated probes to ELISA* plates (R. Giorda et col., 14):

100 µl (per well) of 0,75 pmol/µl probe solution are left 2 hours in incubator at room temperature with stirring.

After washing, 100µl of 5x Denhardt's / 0,02% Na azide solution are placed in each well.

The plates can thus be stored at 4°C and used as and when needed : they just need being washed (three times) and then denatured PCR products are to be dropped in 100µl hybridization buffer; the rest of the protocol is then completed as described above.

Example 2 : Rearrangements detection protocol for a gene with unknown fusion partners.

Total RNAs extracted from the sample cells are to be first treated by ribosomes as follows : 2 µg RNA are to be put into contact with ribozymes (1 µM) in a

buffer solution : $MgCl_2$(20 mM) ; Tris HCl pH 8 (50 mM), to 10 µl volume; the reactive mixture is placed in incubator for 2 hours at 37°C.

The reaction products are collected by precipitation in absolute alcohol(2,5 volumes), with glycogen and sodium acetate (0,3 M final) : 30 min in ice followed by 30 min et 14000 g, 4°C; after rinsing in 75 % alcohol (20 min et 14000 g, 4°C) the precipitates are collected in 10 µl water and subjected to the RT and PCR reactions according to the invention.

Example 3 : MLL gene rearrangements detection

. MLL translocations

The characterization of translocations involving MLL and fusion partners according to the prior art is illustrated by the following table.

Table

MLL Fusion Transcripts

Cytogenetic anomaly	Fusion partner	Proteic family	Leukemia type	Reference
t(10;11)(p12;q23)	*ABI-1*	mABL-intermédiaire 1	LAM	Taki T. *et al.*-1998; (1)
t(1;11)(p32;q23)	AF-1p=eps 15	substrat de EGF Rct	LAM	Bernard O. *et al.*-1994 ; (2)
t(1;11)(q21;q23)	AF-1q	cytokine ?	LAM	Tse W. *et al.*-1995 ; (3)
t(6;11)(q27;q23)*	AF6	myosine/GLGF	T-ALL ou LAM	Prasad R. *et al.* -1993 ; (4)
t(11;19)(q23;p13)*	EEN	domaine SH3	LAM	So C. *et al.* -1997 ; (5)
t(5;11)(q31;q23)	AF-5	domaine GAP + NSL	CMML enfants	Berkhardt A. -1997r ; (6)
t(6;11)*(q21;q23)	AF6 q21	forkhead	MDS/LAM	Bernard O. *et al.* -1997 ; (7)
t(X;11)(q13;q23)	AFX1	forkhead	LAM	Corral J. *et al.* -1993 ; (8)
t(4;11)(q21;q23)*	AF4	riche en ser., pro.	ALL	Gu Y. *et al.* -1992 ; (9)
t(9;11)(p22;q23)	AF9	riche en ser., pro.	LAM	Nakamura T. *et al.*-1993 ; (10)
t(11;19)(q23;p13)	ENL	riche en ser., pro.	ALL	Tkachuk D. *et al.* -1992 ; (11)
t(10;11)(p12;q23)	AF10	doigt de zinc + LZ	LAM	Chaplin T. *et al.* -1995 ; (12)
t(11;17)(q23;q21)	AF17	doigt de zinc + LZ	LAM	Prasad R. *et al.* -1994 ; (13)
t(11;16)(q23;p13)	CBP	adaptateur transcriptionel	LAM secondaire	Taki T. *et al.* -1997 ; (14)
t(11;22)(q23;q13)	p300	adaptateur transcriptionel	LAM secondaire	Ida K. *et al.* -1997 ; (15)
t(11;19)(q23;p13.1)	ELL	fact. d'élongation ARN pol. II	LAM	Thirman M. *et al.* - 1994 ; (16)
t(11;22)(q23;q11,2)	hCDCrel	cycle de division cellulaire	LAM	Megonigal M. *et al.* -1998 ; (17)
(+11)*	MLL	antagoniste de polycomb	LAM	Bernard O. *et al.* - 1995 ; (18)
Aucune	MLL	antagoniste de polycomb	LAM	Schichman S. *et al.* -1994 ; (19)
t(11;15)(q23;q15)	AF-15	aucune homologie	T-ALL	Kuefer M. *et al.* -1997r ; (20)

* = the fusion transcript may be present with a normal caryotype

r = congress' abstract

The research completed on MLL and its partners has highlighted the following facts :

1. Only the chimerical protein obtained by fusion of the NH_2 part of MLL with the C terminal end of the partner seems to be part of the tumorigenic factors

2. In spite of the heterogeneousness of MLL break points, they are all distributed between the gene's exon 5 and exon 11; due to the MLL-specific patterns conservation, the NH_2 parts in fusion proteins are homologous.

3. A very large number of partners exist : at least as many as in the ALL's Igs or TCRs, where known partners account for more than 95 % of MLL translocations described so far. Such partners do not exhibit any actual structural homology ; AF9, AF4 and ENL only are homologous while AF10 and AF17 seems to belong to a new genes family. MLL may be self-associated through a duplication phenomenon

. AML cells assessment

The following results were obtained with leukemia cell lines (human AML) which exhibited particularly 11q23/6q27 rearrangements through cytogenetic assessment. The cell line can thus be used as positive check for the t translocation (6 ; 11).

The relevant cells are part of the ML-2 line (DSM ACC15) cultivated in a RPMI (90%) + SVF 510%) medium. After completion of the culture process, the

cells were frozen in DMSO (5.10^6/ml) for storage or lysed in (Trizol^R) solution to extract nucleic acids.

The TF1 cell line (sampled from a patient with erythroleukoblastosis without 11q23 anomaly) was used for control purpose at various stages in the process (T. Kitamura et al, 21.).

RNAs are to be extracted from the cells as indicated above and subjected to RNase H.

. reverse transcription

The process is the same as described in the example 1 using a 5' sequence, 9 random repeat patterns primer

CGTCGTCGTG AATTCCTAGA TCTTCTAGAT ATGTTNNNNN NNNN

(SEQ ID N° 2, 44 nucletotides, Tm = 84°C).

. amplification

Amplification is obtained as described in the example 1 using the following sens primers :

- on the first cycle, a sequence primer

AGCCCAAGTT TGGTGGTCGC AATATAAAGA AG

(SEQ ID N° 3, 32 nucleotides, Tm = 84°C), and

- on the second cycle an internal sequence primer

GCCGAATTCA TGCCTTCCAA AGCCTACCT

(SEQ ID N° 4, 29 nucleotides, Tm = 86°C), and

a sequence primer used as random primer

CGTCGTCGTG AATTCCTAGA TCTTCTAGAT ATGTT

SUB DH7

(SEQ ID N° 5, 35 nucleotides, Tm = 81°C).

. detection

- hybridization

A specific probe for each MLL partner was defined before the break point of the relevant positive control. The signal/noise ratio obtained by ELISA test reflects the detection efficiency OF each probe. For ENL and duplication, the first value of the ratio corresponds to washing in a full solution, whereas the second value was obtained with ½ diluted solution.

The biotinylated probes used are characterized by Tm comprised betwen 71°C and 75°C, calculated according to the method of the richness in GC by means of a software.

- optical density measurement

The ODs are to be measured for each fusion transcription. The results obtained show that the various partners are detected. Strong signals allow one to easily interpret the results against negative controls.

Moreover, the use of probes defined downstream the break points described in the literature, allows one to locate the molecular event on the relevant gene.

- new partners detection

The RNAs from t(9;11)positive control on Monomac 6) cell line and TF1 line are to be subjected to ribozymes' action.

Two ribozymes with specific enzymatic action of

unaltered MLL gene are used, their cleaving sites are located downstream of the break points region. Such ribozymes respective sequences are as follows :

SUB D5

- ribozyme 1 : CUCCAGCUGA UGAGUCCGUG AGGACGAAAC CUUUGG (SEQ ID N° 6)

SUB D6

- ribozyme 2 : CUGGAAUCUG AUGAGUCCGU GAGGACGAAA UUUUCUUC (SEQ ID N° 7).

Underscored sequences correspond to MLL complimentary sequences about the cleavage points and the plain sequences mean the unpaired sequences leading to the formation of secondary structures required by the ribozymes' catalyst action. Cleaving occurs on the 3' end of the nucleotide following the uracil make up to adenine .

The reaction products were converted into cDNA, and then subjected to amplification by means of a pair of primers located on either side of the cutting points.

Therefore, the invention provides the molecular tools and a diagnostic method which can be used on a large number of patients to identify the various MLL partners and relevant break points, and to better understand the development mechanisms of pathologies associated with genes rearrangement, e.g. : leukemiagenesis mechanisms underlying the MLL gene rearrangement.

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